

1U 102 R1.ST25  
SEQUENCE LISTING

<110> OriGene Technologies, Inc.  
<120> Angiogenesis Dehydrogenase Gene  
<130> 1U 102 R1  
<160> 4  
<170> PatentIn version 3.1

<210> 1  
<211> 3727  
<212> DNA  
<213> homo sapiens

<220>  
<221> CDS  
<222> (28)..(1689)  
<223>

<400> 1  
gtgcgtcggc ggtgggtggg tggtaag atg gcg gct gtg agt ctg cgg ctc ggc 54  
Met Ala Ala Val Ser Leu Arg Leu Gly  
1 5  
gac ttg gtg tgg ggg aaa ctc ggc cga tat cct cct tgg cca gga aag 102  
Asp Leu Val Trp Gly Lys Leu Gly Arg Tyr Pro Pro Trp Pro Gly Lys  
10 15 20 25  
att gtt aat cca cca aag gac ttg aag aaa cct cgc gga aag aaa tgc 150  
Ile Val Asn Pro Pro Lys Asp Leu Lys Pro Arg Gly Lys Lys Cys  
30 35 40  
ttc ttt gtg aaa ttt ttt gga aca gaa gat cat gcc tgg atc aaa gtg 198  
Phe Phe Val Lys Phe Phe Gly Thr Glu Asp His Ala Trp Ile Lys Val  
45 50 55  
gaa cag ctg aag cca tat cat gct cat aaa gag gaa atg ata aaa att 246  
Glu Gln Leu Lys Pro Tyr His Ala His Lys Glu Glu Met Ile Lys Ile  
60 65 70  
aac aag ggt aaa cga ttc cag caa gcg gta gat gct gtc gaa gag ttc 294  
Asn Lys Gly Lys Arg Phe Gln Gln Ala Val Asp Ala Val Glu Glu Phe  
75 80 85  
ctc agg aga gcc aaa ggg aaa gac cag acg tca tcc cac aat tct tct 342  
Leu Arg Arg Ala Lys Gly Lys Asp Gln Thr Ser Ser His Asn Ser Ser  
90 95 100 105  
gat gac aag aat cga cgt aat tcc agt gag gag aga agt agg cca aac 390  
Asp Asp Lys Asn Arg Arg Asn Ser Ser Glu Glu Arg Ser Arg Pro Asn  
110 115 120  
tca ggt gat gag aag cgc aaa ctt agc ctg tct gaa ggg aag gtg aag 438  
Ser Gly Asp Glu Lys Arg Lys Leu Ser Leu Ser Glu Gly Lys Val Lys  
125 130 135  
aag aac atg gga gaa gga aag aag agg gtg tct tca ggc tct tca gag 486  
Lys Asn Met Gly Glu Gly Lys Lys Arg Val Ser Ser Gly Ser Ser Glu  
140 145 150  
aga ggc tcc aaa tcc cct ctg aaa aga gcc caa gag caa agt ccc cgg 534  
Arg Gly Ser Lys Ser Pro Leu Lys Arg Ala Gln Glu Gln Ser Pro Arg  
155 160 165  
aag cgg ggt cgg ccc cca aag gat gag aag gat ctc acc atc ccg gag 582  
Lys Arg Gly Arg Pro Pro Lys Asp Glu Lys Asp Leu Thr Ile Pro Glu  
170 175 180 185  
tct agt acc gtg aag ggg atg atg gcc gga ccg atg gcc gcg ttt aaa 630  
Ser Ser Thr Val Lys Gly Met Met Ala Gly Pro Met Ala Ala Phe Lys

190

195

200

tgg cag cca acc gca agc gag cct gtt aaa gat gca gat cct cat ttc Trp Gln Pro Thr Ala Ser Glu Pro Val Lys Asp Ala Asp Pro His Phe 205 210 215	678
cat cat ttc ctg cta agc caa aca gag aag cca gct gtc tgt tac cag His His Phe Leu Leu Ser Gln Thr Glu Lys Pro Ala Val Cys Tyr Gln 220 225 230	726
gca atc acg aag aag ttg aaa ata tgt gaa gag gaa act ggc tcc acc Ala Ile Thr Lys Lys Leu Lys Ile Cys Glu Glu Thr Gly Ser Thr 235 240 245	774
tcc atc cag gca gct gac agc aca gcc gtg aat ggc agc atc aca ccc Ser Ile Gln Ala Ala Asp Ser Thr Ala Val Asn Gly Ser Ile Thr Pro 250 255 260 265	822
aca gac aaa aag ata gga ttt ttg ggc ctt ggt ctc atg gga agt gga Thr Asp Lys Ile Gly Phe Leu Gly Leu Gly Leu Met Gly Ser Gly 270 275 280	870
atc gtc tcc aac ttg cta aaa atg ggt cac aca gtg act gtc tgg aac Ile Val Ser Asn Leu Leu Lys Met Gly His Thr Val Thr Val Trp Asn 285 290 295	918
cgc act gca gag aaa tgt gat ttg ttc atc cag gag ggg gcc cgt ctg Arg Thr Ala Glu Lys Cys Asp Leu Phe Ile Gln Glu Gly Ala Arg Leu 300 305 310	966
gga aga acc ccc gct gaa gtc gtc tca acc tgc gac atc act ttc gcc Gly Arg Thr Pro Ala Glu Val Val Ser Thr Cys Asp Ile Thr Phe Ala 315 320 325	1014
tgc gtg tcg gat ccc aag gcg gcc aag gac ctg gtg ctg ggc ccc agt Cys Val Ser Asp Pro Lys Ala Ala Lys Asp Leu Val Leu Gly Pro Ser 330 335 340 345	1062
ggg gtg ctg caa ggg atc cgc cct ggg aag tgc tac gtg gac atg tca Gly Val Leu Gln Gly Ile Arg Pro Gly Lys Cys Tyr Val Asp Met Ser 350 355 360	1110
aca gtg gac gac acc gtc act gag ctg gcc cag gtg att gtg tcc Thr Val Asp Ala Asp Thr Val Thr Glu Leu Ala Gln Val Ile Val Ser 365 370 375	1158
agg ggg ggg cgc ttt ctg gaa gcc ccc gtc tca ggg aat cag cag ctg Arg Gly Gly Arg Phe Leu Glu Ala Pro Val Ser Gly Asn Gln Gln Leu 380 385 390	1206
tct aat gac ggg atg ttg gtg atc tta gcg gct gga gac agg ggc tta Ser Asn Asp Gly Met Leu Val Ile Leu Ala Ala Gly Asp Arg Gly Leu 395 400 405	1254
tat gag gac tgc agc agc tgc ttc cag gcg atg ggg aag acc tcc ttc Tyr Glu Asp Cys Ser Ser Cys Phe Gln Ala Met Gly Lys Thr Ser Phe 410 415 420 425	1302
ttc cta ggt gaa gtg ggc aat gca gcc aag atg atg ctg atc gtg aac Phe Leu Gly Glu Val Gly Asn Ala Ala Lys Met Met Leu Ile Val Asn 430 435 440	1350
atg gtc caa ggg agc ttc atg gcc act att gcc gag ggg ctg acc ctg Met Val Gln Gly Ser Phe Met Ala Thr Ile Ala Glu Gly Leu Thr Leu 445 450 455	1398
gcc cac gtg aca ggc cag tcc cag cag aca ctc ttg gac atc ctc aat Ala His Val Thr Gly Gln Ser Gln Gln Thr Leu Leu Asp Ile Leu Asn 460 465 470	1446
cag gga cag ttg gcc agc atc ttc ctg gac cag aag tgc caa aat atc Gln Gly Gln Leu Ala Ser Ile Phe Leu Asp Gln Lys Cys Gln Asn Ile 475 480 485	1494

	1U 102 R1.ST25	
ctg caa gga aac ttt aag cct gat ttc tac ctg aaa tac att cag aag		1542
Leu Gln Gly Asn Phe Lys Pro Asp Phe Tyr Leu Lys Tyr Ile Gln Lys		
490 495 500 505		
gat ctc cgc tta gcc att gcg ctg ggt gat gcg gtc aac cat ccg act		1590
Asp Leu Arg Leu Ala Ile Ala Leu Gly Asp Ala Val Asn His Pro Thr		
510 515 520		
ccc atg gca gct gca gca aat gag gtg tac aaa aga gcc aag gcg ctg		1638
Pro Met Ala Ala Ala Asn Glu Val Tyr Lys Arg Ala Lys Ala Leu		
525 530 535		
gac cag tcc gac aac gat atg tcc gcc gtg tac cga gcc tac ata cac		1686
Asp Gln Ser Asp Asn Asp Met Ser Ala Val Tyr Arg Ala Tyr Ile His		
540 545 550		
taa gctgtcgaca ccccgccctc accccctccaa tccccctct gacccctct		1739
tcctcacatg gggtcggggg cctggagtt cattctggac cagcccacct atctccattt		1799
cctttatac agactttgag acttgccatc agcacagcac acagcagcac cttccctgt		1859
ggccgggtgg ggaggggaca agtgtcagca ggattggcgt gtggaaagc tctttagctg		1919
ggactggcc cccggacga ggtggctgtg tttcacacaca cacacacacaca cacacacaca		1979
ggctctcgcc ccaggataga agctgcccag aaactgctgc ctggctttt ttctccgag		2039
tttgtcttat ctcaaaccctt ttccagtcaa ggaactagaa tcagcaacga gagttgaaag		2099
ccttccacaca gttcccccaga ggcgaagag gctgttagtca tggccatc cccactgg		2159
ttccctacaa ggagaggct tggcccaaga tgagccagta cagactccag acagagggc		2219
ccttggggcc ctccaaacctc aggtgatgag ctgagaaaga tggcacatc taagcgttca		2279
gtgtgcaccc agcgctccat agacgcctt gtgaactgaa aagagactgg cagagtcccg		2339
agaagatggg gcccggctt tccaggagtt gcagcaagca gcccgcgtgc aggtgagcat		2399
ggaggccgg ccctcaccgc ctcaagcca tggccatc gcaactgcca cagccggcgc		2459
tcgtctccctt ctaggtgtt ttagtattt gatttgcatt ccattccctt ggaggagtc		2519
ctcaggccca ctatgtatg gccaagagga gtgggggtt ggggcgttcc ttctgtttc		2579
cgttaggcca cagactttc acctggctt gaagagccac tcttacctcg gtccctcc		2639
agtggtccca ctttctccac cttggccgtc caagtccctt gcatgcccac cgctctccat		2699
cctcccttctt cttcccttcc ctccgggtt gacagtattt ctttctgtct gtccctttgg		2759
cccagaccca gctgaccaa cgtgagcat ttcttaggt cagctttga tacggaaacg		2819
agtgtttca ctccagccag catcatggtc ttccgggtt cccggggccgg gggctgtcg		2879
ggagggaaaga gaactggcc tggacttaccc gaaactgactg gcccgttgc gttggctgg		2939
gacatccatggccca agggccatata ttgtccctt gatagggac cggggggggc ttggatgtt		2999
gaaaaaaaaa aagtatccca agggatgtca gttttttatc cctctgtcg gttggattt		3059
tccaaaatca taatttgcag aagggaaaggcc agcatttatg atgcaatatg taattatata		3119
tagggggcc acactaggcc ggggtccctt cccctcaca gctttggccc ctttcagaga		3179
ttagaaactg gtttagagga ttgcagaaga cgtgggggg gggggcaggaa aagatgcctg		3239
tcgggtttttt agcacagttt atttcactgg gatggtaag catttcgtc tgaacacaaa		3299
gcctgttcta gtcctggcgg aacacactgg ggggtggggc gggggaaagat gcggtatga		3359
aaccggtag tcaatttgtt cttatattt ttgacaattc tggtaatgtt cttttatgtt		3419

	10 102 R1.ST25	
atatttctgt ttaagctatt tcaccttct tttgaaatcc ttcccttta aggagaaaat	3479	
gtgacacttg tgaaaaagct tgtaagaaag cccctccctt ttttctttaa acctttaat	3539	
gacaaatcta ggttaattaaag gttgtgaatt tttatttttt ctgggtttttt aatgaacatt	3599	
tgtcttcag aataggattg tgtgataatg tttaaatggc aaaaacaaaa catgatttg	3659	
tgcaatttaac aaagctactg caagaaaaat aaaacacttc ttggtaacac aaaaaaaaaa	3719	
aaaaaaaaaa	3727	

<210> 2  
<211> 553  
<212> PRT  
<213> homo sapiens

<400> 2

Met Ala Ala Val Ser Leu Arg Leu Gly Asp Leu Val Trp Gly Lys Leu  
1 5 10 15

Gly Arg Tyr Pro Pro Trp Pro Gly Lys Ile Val Asn Pro Pro Lys Asp  
20 25 30

Leu Lys Lys Pro Arg Gly Lys Lys Cys Phe Phe Val Lys Phe Phe Gly  
35 40 45

Thr Glu Asp His Ala Trp Ile Lys Val Glu Gln Leu Lys Pro Tyr His  
50 55 60

Ala His Lys Glu Glu Met Ile Lys Ile Asn Lys Gly Lys Arg Phe Gln  
65 70 75 80

Gln Ala Val Asp Ala Val Glu Glu Phe Leu Arg Arg Ala Lys Gly Lys  
85 90 95

Asp Gln Thr Ser Ser His Asn Ser Ser Asp Asp Lys Asn Arg Arg Asn  
100 105 110

Ser Ser Glu Glu Arg Ser Arg Pro Asn Ser Gly Asp Glu Lys Arg Lys  
115 120 125

Leu Ser Leu Ser Glu Gly Lys Val Lys Lys Asn Met Gly Glu Gly Lys  
130 135 140

Lys Arg Val Ser Ser Gly Ser Ser Glu Arg Gly Ser Lys Ser Pro Leu  
145 150 155 160

Lys Arg Ala Gln Glu Gln Ser Pro Arg Lys Arg Gly Arg Pro Pro Lys  
165 170 175

Asp Glu Lys Asp Leu Thr Ile Pro Glu Ser Ser Thr Val Lys Gly Met  
180 185 190

Met Ala Gly Pro Met Ala Ala Phe Lys Trp Gln Pro Thr Ala Ser Glu  
195 200 205

Pro Val Lys Asp Ala Asp Pro His Phe His His Phe Leu Leu Ser Gln  
210 215 220

Thr Glu Lys Pro Ala Val Cys Tyr Gln Ala Ile Thr Lys Lys Leu Lys  
 225 230 235 240

Ile Cys Glu Glu Glu Thr Gly Ser Thr Ser Ile Gln Ala Ala Asp Ser  
 245 250 255

Thr Ala Val Asn Gly Ser Ile Thr Pro Thr Asp Lys Lys Ile Gly Phe  
 260 265 270

Leu Gly Leu Gly Leu Met Gly Ser Gly Ile Val Ser Asn Leu Leu Lys  
 275 280 285

Met Gly His Thr Val Thr Val Trp Asn Arg Thr Ala Glu Lys Cys Asp  
 290 295 300

Leu Phe Ile Gln Glu Gly Ala Arg Leu Gly Arg Thr Pro Ala Glu Val  
 305 310 315 320

Val Ser Thr Cys Asp Ile Thr Phe Ala Cys Val Ser Asp Pro Lys Ala  
 325 330 335

Ala Lys Asp Leu Val Leu Gly Pro Ser Gly Val Leu Gln Gly Ile Arg  
 340 345 350

Pro Gly Lys Cys Tyr Val Asp Met Ser Thr Val Asp Ala Asp Thr Val  
 355 360 365

Thr Glu Leu Ala Gln Val Ile Val Ser Arg Gly Gly Arg Phe Leu Glu  
 370 375 380

Ala Pro Val Ser Gly Asn Gln Gln Leu Ser Asn Asp Gly Met Leu Val  
 385 390 395 400

Ile Leu Ala Ala Gly Asp Arg Gly Leu Tyr Glu Asp Cys Ser Ser Cys  
 405 410 415

Phe Gln Ala Met Gly Lys Thr Ser Phe Phe Leu Gly Glu Val Gly Asn  
 420 425 430

Ala Ala Lys Met Met Leu Ile Val Asn Met Val Gln Gly Ser Phe Met  
 435 440 445

Ala Thr Ile Ala Glu Gly Leu Thr Leu Ala His Val Thr Gly Gln Ser  
 450 455 460

Gln Gln Thr Leu Leu Asp Ile Leu Asn Gln Gly Gln Leu Ala Ser Ile  
 465 470 475 480

Phe Leu Asp Gln Lys Cys Gln Asn Ile Leu Gln Gly Asn Phe Lys Pro  
 485 490 495

Asp Phe Tyr Leu Lys Tyr Ile Gln Lys Asp Leu Arg Leu Ala Ile Ala  
 500 505 510

1U 102 R1.ST25

Leu Gly Asp Ala Val Asn His Pro Thr Pro Met Ala Ala Ala Asn  
515 520 525

Glu Val Tyr Lys Arg Ala Lys Ala Leu Asp Gln Ser Asp Asn Asp Met  
530 535 540

Ser Ala Val Tyr Arg Ala Tyr Ile His  
545 550

<210> 3  
<211> 547  
<212> PRT  
<213> homo sapiens

<400> 3

Met Ala Ala Val Ser Leu Arg Leu Gly Asp Leu Val Trp Gly Lys Leu  
1 5 10 15

Gly Arg Tyr Pro Pro Trp Pro Gly Lys Ile Val Asn Pro Pro Lys Asp  
20 25 30

Leu Lys Lys Pro Arg Gly Lys Lys Cys Phe Phe Val Lys Phe Phe Gly  
35 40 45

Thr Glu Asp His Ala Trp Ile Lys Val Glu Gln Leu Lys Pro Tyr His  
50 55 60

Ala His Lys Glu Glu Met Ile Lys Ile Asn Lys Gly Lys Arg Phe Gln  
65 70 75 80

Gln Ala Val Asp Ala Val Glu Glu Phe Leu Arg Arg Ala Lys Gly Lys  
85 90 95

Asp Gln Thr Ser Ser His Asn Ser Ser Asp Asp Lys Asn Arg Arg Asn  
100 105 110

Ser Ser Glu Glu Arg Ser Arg Pro Asn Ser Gly Asp Glu Lys Arg Lys  
115 120 125

Leu Ser Leu Ser Glu Gly Lys Val Lys Lys Asn Met Gly Glu Gly Lys  
130 135 140

Lys Arg Val Ser Ser Gly Ser Ser Glu Arg Gly Ser Lys Ser Pro Leu  
145 150 155 160

Lys Arg Ala Gln Glu Gln Ser Pro Arg Lys Arg Gly Arg Pro Pro Lys  
165 170 175

Asp Glu Lys Asp Leu Thr Ile Pro Glu Ser Ser Thr Val Lys Gly Met  
180 185 190

Met Ala Gly Pro Met Ala Ala Phe Lys Trp Gln Pro Thr Ala Ser Glu  
195 200 205

Pro Val Lys Asp Ala Asp Pro His Phe His His Phe Leu Leu Ser Gln  
210 215 220

1U 102 R1.ST25

Thr Glu Lys Pro Ala Val Cys Tyr Gln Ala Ile Thr Lys Lys Leu Lys  
225 230 235 240

Ile Cys Glu Glu Glu Thr Gly Ser Thr Ser Ile Gln Ala Ala Asp Ser  
245 250 255 260

Thr Ala Val Asn Gly Ser Ile Thr Pro Thr Asp Lys Lys Ile Gly Phe  
260 265 270

Leu Gly Leu Gly Leu Met Gly Ser Gly Ile Val Ser Asn Leu Leu Lys  
275 280 285

Met Gly His Thr Val Thr Val Trp Asn Arg Thr Ala Glu Lys Glu Gly  
290 295 300

Ala Arg Leu Gly Arg Thr Pro Ala Glu Val Val Ser Thr Cys Asp Ile  
305 310 315 320

Thr Phe Ala Cys Val Ser Asp Pro Lys Ala Ala Lys Asp Leu Val Leu  
325 330 335

Gly Pro Ser Gly Val Leu Gln Gly Ile Arg Pro Gly Lys Cys Tyr Val  
340 345 350

Asp Met Ser Thr Val Asp Ala Asp Thr Val Thr Glu Leu Ala Gln Val  
355 360 365

Ile Val Ser Arg Gly Gly Arg Phe Leu Glu Ala Pro Val Ser Gly Asn  
370 375 380

Gln Gln Leu Ser Asn Asp Gly Met Leu Val Ile Leu Ala Ala Gly Asp  
385 390 395 400

Arg Gly Leu Tyr Glu Asp Cys Ser Ser Cys Phe Gln Ala Met Gly Lys  
405 410 415

Thr Ser Phe Phe Leu Gly Glu Val Gly Asn Ala Ala Lys Met Met Leu  
420 425 430

Ile Val Asn Met Val Gln Gly Ser Phe Met Ala Thr Ile Ala Glu Gly  
435 440 445

Leu Thr Leu Ala Gln Val Thr Gly Gln Ser Gln Gln Thr Leu Leu Asp  
450 455 460

Ile Leu Asn Gln Gln Leu Ala Ser Ile Phe Leu Asp Gln Lys Cys  
465 470 475 480

Gln Asn Ile Leu Gln Gly Asn Phe Lys Pro Asp Phe Tyr Leu Lys Tyr  
485 490 495

Ile Gln Lys Asp Leu Arg Leu Ala Ile Ala Leu Gly Asp Ala Val Asn  
500 505 510

His Pro Thr Pro Met Ala Ala Ala Asn Glu Val Tyr Lys Arg Ala  
Page 7

515

520

1U 102 R1.ST25  
525

Lys Ala Leu Asp Gln Ser Asp Asn Asp Met Ser Ala Val Tyr Arg Ala  
530 535 540

Tyr Ile His  
545

<210> 4  
<211> 276  
<212> PRT  
<213> homo sapiens  
<400> 4

Met Gly Ser Gly Ile Val Ser Asn Leu Leu Lys Met Gly His Thr Val  
1 5 10 15

Thr Val Trp Asn Arg Thr Ala Glu Lys Cys Asp Leu Phe Ile Gln Glu  
20 25 30

Gly Ala Arg Leu Gly Arg Thr Pro Ala Glu Val Val Ser Thr Cys Asp  
35 40 45

Ile Thr Phe Ala Cys Val Ser Asp Pro Lys Ala Ala Lys Asp Leu Val  
50 55 60

Leu Gly Pro Ser Gly Val Leu Gln Gly Ile Arg Pro Gly Lys Cys Tyr  
65 70 75 80

Val Asp Met Ser Thr Val Asp Ala Asp Thr Val Thr Glu Leu Ala Gln  
85 90 95

Val Ile Val Ser Arg Gly Gly Arg Phe Leu Glu Ala Pro Val Ser Gly  
100 105 110

Asn Gln Gln Leu Ser Asn Asp Gly Met Leu Val Ile Leu Ala Ala Gly  
115 120 125

Asp Arg Gly Leu Tyr Glu Asp Cys Ser Ser Cys Phe Gln Ala Met Gly  
130 135 140

Lys Thr Ser Phe Phe Leu Gly Glu Val Gly Asn Ala Ala Lys Met Met  
145 150 155 160

Leu Ile Val Asn Met Val Gln Gly Ser Phe Met Ala Thr Ile Ala Glu  
165 170 175

Gly Leu Thr Leu Ala His Val Thr Gly Gln Ser Gln Gln Thr Leu Leu  
180 185 190

Asp Ile Leu Asn Gln Gly Gln Leu Ala Ser Ile Phe Leu Asp Gln Lys  
195 200 205

Cys Gln Asn Ile Leu Gln Gly Asn Phe Lys Pro Asp Phe Tyr Leu Lys  
210 215 220

1U 102 R1.ST25

Tyr Ile Gln Lys Asp Leu Arg Leu Ala Ile Ala Leu Gly Asp Ala Val  
225 230 235 240

Asn His Pro Thr Pro Met Ala Ala Ala Asn Glu Val Tyr Lys Arg  
245 250 255

Ala Lys Ala Leu Asp Gln Ser Asp Asn Asp Met Ser Ala Val Tyr Arg  
260 265 270

Ala Tyr Ile His  
275